

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/ 628,525A  
Source: IFW 16  
Date Processed by STIC: 7-6-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 07/06/2005

PATENT APPLICATION: US/10/628,525A

TIME: 12:29:49

Input Set : A:\1505604.app

Output Set: N:\CRF4\07062005\J628525A.raw

(pg. 6)

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3 <110> APPLICANT: KEELING, PETER
4   GAUN, HANPLING
6 <120> TITLE OF INVENTION: STARCH ENCAPSULATION
8 <130> FILE REFERENCE: 15056-04
10 <140> CURRENT APPLICATION NUMBER: 10/628,525A
11 <141> CURRENT FILING DATE: 2003-07-28
13 <150> PRIOR APPLICATION NUMBER: 09/625,406
14 <151> PRIOR FILING DATE: 2000-07-25
16 <150> PRIOR APPLICATION NUMBER: 08/941,445
17 <151> PRIOR FILING DATE: 1997-09-30
19 <150> PRIOR APPLICATION NUMBER: 60/026,855
20 <151> PRIOR FILING DATE: 1996-09-30
22 <160> NUMBER OF SEQ ID NOS: 40
24 <170> SOFTWARE: PatentIn Ver. 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 31
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
33   primer
35 <400> SEQUENCE: 1
36 gactagtcat atggtgagca agggcgagga g                               31
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 36
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42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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49 ctatgcttc atagcttgt acagctcgtc catgcc                             36
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 39
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
59   primer
61 <400> SEQUENCE: 3
62 ctatgcttg gccatggcct tgtacagctc gtccatgcc                         39
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 4800

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67 <212> TYPE: DNA
68 <213> ORGANISM: Zea mays
70 <220> FEATURE:
71 <221> NAME/KEY: CDS
72 <222> LOCATION: (1449) .. (1553)
74 <220> FEATURE:
75 <221> NAME/KEY: CDS
76 <222> LOCATION: (1685) .. (1765)
78 <220> FEATURE:
79 <221> NAME/KEY: CDS
80 <222> LOCATION: (1860) .. (1958)
82 <220> FEATURE:
83 <221> NAME/KEY: CDS
84 <222> LOCATION: (2055) .. (2144)
86 <220> FEATURE:
87 <221> NAME/KEY: CDS
88 <222> LOCATION: (2226) .. (2288)
90 <220> FEATURE:
91 <221> NAME/KEY: CDS
92 <222> LOCATION: (2412) .. (2513)
94 <220> FEATURE:
95 <221> NAME/KEY: CDS
96 <222> LOCATION: (2651) .. (2761)
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (2859) .. (3101)
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112 <222> LOCATION: (3793) .. (3879)
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120 <222> LOCATION: (4227) .. (4340)
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125 tttggtgaag ctctgctcgc agctgtccgg ctcttggac gttcgtgtgg cagattcatc 120
127 tgttgtctcg tctcctgtgc ttcttgggta gcttgtgtag tggagctgac atggtctgag 180
129 caggcttaaa atttgctcgt agacgaggag taccagcaca gcacgttgcg gatttctctg 240
131 cctgtgaagt gcaacgtcta ggattgtcac acgccttggc cgcgtcgcgt cgcgtcgcgt 300
133 cgatgcggtg gtgagcagag cagcaacagc tgggcggccc aacgttggct tccgtgtctt 360
135 cgctgtacgt acgcgcgcgc cggggacacg cagcagagag cggagagcga gccgtgcacg 420

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137 gggaggtggt gtggaagtgg agcgcgcgcgc ccggccgcgc gcgcccgggtg ggcaacccaa 480
139 aagtaccacac gacaagcgaa ggcgcgcaaag cgatccaagc tccggaacgc aacagcatgc 540
141 gtcgcgtcgg agagccagcc acaagcagcc gagaaccgaa ccggtgggcg acgcgtcatg 600
143 ggacggacgc gggcgacgct tccaaacggg ccacgtacgc cggcgtgtgc gtgcgtgcag 660
145 acgacaagcc aaggcgaggc agccccgat cgggaaagcg ttttgggcgc gagcgttggc 720
147 gtgcgggtca gtcgctgggtg cgcagtgcgc gggggaacgg gtatcgtggg gggcgcgggc 780
149 ggaggagagc gtggcgaggg ccgagagcag cgcgcggccg ggtcacgcaa cgcgccccac 840
151 gtactgccct cccctccgc gcgcgctaga aataccgagg cctggaccgg gggggggccc 900
153 cgtcacatcc atccatcgac cgatcgatcg ccacagccaa caccaccgc cgaggcgacg 960
155 cgacagccgc caggaggaag gaataaactc actgccagcc agtgaagggg gagaagtgt 1020
157 ctgctccgtc gaccagtgcg cgcaccgccc ggcagggtcg ctcattctgt cgacgaccag 1080
159 gttctgttcc gttccgatcc gatccgatcc tgtccttgag tttcgtccag atcctggcgc 1140
161 gtatctgcgt gtttgatgat ccaggttctt cgaacctaaa tctgtccgtg cacacgtctt 1200
163 ttctctctct cctacgcagt ggattaatcg gcatggcggc tctggccacg tcgcagctcg 1260
165 tcgcaacgcg cgcgcggcctg ggcgtcccg acgcgtccac gttccgcgcg ggcgcgcgcg 1320
167 agggcctgag gggggcccg gcgtcggcgg cggcggaacac gctcagcatg cggaccagcg 1380
169 cgcgcgcggc gccagggcac cagcagcagg cgcgcgcggg gggcagggtc ccgtcgtcgt 1440
171 tcgtgtgc gcc agc gcc ggc atg aac gtc gtc ttc gtc ggc gcc gag atg 1490
172 Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met
173 1 5 10
175 gcg ccg tgg agc aag acc ggc ggc ctc ggc gac gtc ctc ggc ggc ctg 1538
176 Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu
177 15 20 25 30
179 ccg ccg gcc atg gcc gtaagcgcgc gcaccgagac atgcatccgt tggatcgcgt 1593
180 Pro Pro Ala Met Ala
181 35
183 cttcttcgtg ctcttgccgc gtgcatgatg catgtgttct ctcctggctt gtgttcgtgt 1653
185 atgtgacgtg tttgttcggg catgcatgca g gcg aac ggg cac cgt gtc atg 1705
186 Ala Asn Gly His Arg Val Met
187 40
189 gtc gtc tct ccc cgc tac gac cag tac aag gac gcc tgg gac acc agc 1753
190 Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser
191 45 50 55
193 gtc gtg tcc gag gtacggccac cgagaccaga ttcagatcac agtcacacac 1805
194 Val Val Ser Glu
195 60
197 accgtcatat gaacctttct ctgctctgat gcctgcaact gcaaattgcat gcag atc 1862
198 Ile
200 aag atg gga gac ggg tac gag acg gtc agg ttc ttc cac tgc tac aag 1910
201 Lys Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys
202 65 70 75
204 cgc gga gtg gac cgc gtg ttc gtt gac cac cca ctg ttc ctg gag agg 1958
205 Arg Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg
206 80 85 90 95
208 gtgagacgag atctgatcac tcgatacgca attaccaccc cattgtaagc agttacagtg 2018
210 agcttttttt cccccggcc tggctcgtgg tttcag gtt tgg gga aag acc gag 2072
211 Val Trp Gly Lys Thr Glu
212 100
214 gag aag atc tac ggg cct gtc gct gga acg gac tac agg gac aac cag 2120

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215 Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln
216          105          110          115
218 ctg cgg ttc agc ctg cta tgc cag gtcaggatgg cttggtacta caacttcata 2174
219 Leu Arg Phe Ser Leu Leu Cys Gln
220          120          125
222 tcattctgtat gcagcagtat aactgatga gaaatgcatg ctgttctgca g gca gca 2231
223                               Ala Ala
225 ctt gaa gct cca agg atc ctg agc ctc aac aac aac cca tac ttc tcc 2279
226 Leu Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser
227          130          135          140
229 gga cca tac ggtaagagtt gcagtcttcg tatatatatc tggtgagctc 2328
230 Gly Pro Tyr
231          145
233 gagaatcttc acaggaagcg gccatcaga cggactgtca ttttactg actactgctg 2388
235 ctgctcttcg tccatccata caa ggg gag gac gtc gtg ttc gtc tgc aac gac 2441
236                               Gly Glu Asp Val Val Phe Val Cys Asn Asp
237                               150          155
239 tgg cac acc ggc cct ctc tgc tgc tac ctc aag agc aac tac cag tcc 2489
240 Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln Ser
241          160          165          170
243 cac ggc atc tac agg gac gca aag gttgccttct ctgaactgaa caacgccgtt 2543
244 His Gly Ile Tyr Arg Asp Ala Lys
245          175          180
247 ttcgttctcc atgctcgtat atacctcgtc tggtagtggg ggtgcttctc tgagaaacta 2603
249 actgaaactg actgcatgctc tgtctgacca tcttcacgta ctaccag acc gct ttc 2659
250                               Thr Ala Phe
252 tgc atc cac aac atc tcc tac cag ggc cgg ttc gcc ttc tcc gac tac 2707
253 Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
254          185          190          195
256 ccg gag ctg aac ctc ccg gag aga ttc aag tgc tcc ttc gat ttc atc 2755
257 Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
258 200          205          210          215
260 gac ggg tctgttttcc tgcgtgcatg tgaacattca tgaatggtaa cccacaactg 2811
261 Asp Gly
263 ttcgcgtcct gctgggttcat tatctgacct gattgcatta ttgcagc tac gag aag 2867
264                               Tyr Glu Lys
265                               220
267 ccc gtg gaa ggc cgg aag atc aac tgg atg aag gcc ggg atc ctc gag 2915
268 Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly Ile Leu Glu
269          225          230          235
271 gcc gac agg gtc ctc acc gtc agc ccc tac tac gcc gag gag ctc atc 2963
272 Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile
273          240          245          250
275 tcc ggc atc gcc agg ggc tgc gag ctc gac aac atc atg cgc ctc acc 3011
276 Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr
277          255          260          265
279 ggc atc acc ggc atc gtc aac ggc atg gag gtc agc gag tgg gac ccc 3059
280 Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro
281          270          275          280

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283 agc agg gac aag tac atc gcc gtg aag tac gac gtg tcg acg          3101
284 Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr
285 285                290                295
287 gtgagctggc tagctctgat tctgtctgcct ggtcctcctg ctcacatcatgc tgggttcggta 3161
289 ctgacgcggc aagtgtacgt acgtgcgtgc gacggtgggtg tccggttcag gcc gtg      3217
290                               Ala Val
291                               300
293 gag gcc aag gcg ctg aac aag gag gcg ctg cag gcg gag gtc ggg ctc      3265
294 Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu
295                305                310                315
297 ccg gtg gac cgg aac atc ccg ctg gtg gcg ttc atc ggc agg ctg gaa      3313
298 Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu
299                320                325                330
301 gag cag aag ggc ccc gac gtc atg gcg gcc gcc atc ccg cag ctc atg      3361
302 Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met
303                335                340                345
305 gag atg gtg gag gac gtg cag atc gtt ctg ctg gtacgtgtgc gccggccgcc 3414
306 Glu Met Val Glu Asp Val Gln Ile Val Leu Leu
307                350                355
309 acccggctac tacatgcgtg tctcgttcgt tctactggaa catgcgtgtg agcaacgcga 3474
311 tggataatgc tgcag ggc acg ggc aag aag aag ttc gag cgc atg ctc atg      3525
312                               Gly Thr Gly Lys Lys Lys Phe Glu Arg Met Leu Met
313                360                365                370
315 agc gcc gag gag aag ttc cca ggc aag gtg cgc gcc gtg gtc aag ttc      3573
316 Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val Lys Phe
317                375                380                385
319 aac gcg gcg ctg gcg cac cac atc atg gcc ggc gcc gac gtg ctc gcc      3621
320 Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp Val Leu Ala
321                390                395                400
323 gtc acc agc cgc ttc gag ccc tgc ggc ctc atc cag ctg cag ggg atg      3669
324 Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln Gly Met
325                405                410                415
327 cga tac gga acg gtacgagaga aaaaaaaaaat cctgaatcct gacgagaggg      3721
328 Arg Tyr Gly Thr
329 420
331 acagagacag attatgaatg cttcatcgat ttgaattgat tgatcgatgt ctcccgtgc      3781
333 gactcttgca g ccc tgc gcc tgc gcg tcc acc ggt gga ctc gtc gac acc      3831
334                               Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu Val Asp Thr
335                425                430                435
337 atc atc gaa ggc aag acc ggg ttc cac atg ggc cgc ctc agc gtc gac      3879
338 Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu Ser Val Asp
339                440                445                450
341 gtaagcctag ctctgccatg ttctttcttc ttctttcttg tatgtatgta tgaatcagca 3939
343 ccgccgttct tgtttcgtcg tcgtcctctc ttcccag tgt aac gtc gtg gag ccg      3994
344                               Cys Asn Val Val Glu Pro
345                               455
347 gcg gac gtc aag aag gtg gcc acc aca ttg cag cgc gcc atc aag gtg      4042
348 Ala Asp Val Lys Lys Val Ala Thr Thr Leu Gln Arg Ala Ile Lys Val
349                460                465                470

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/628,525A

DATE: 07/06/2005  
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Input Set : A:\1505604.app  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; Xaa Pos. 17

Seq#:39; Xaa Pos. 2

**VERIFICATION SUMMARY**

DATE: 07/06/2005

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Input Set : A:\1505604.app

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L:3057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16

L:3093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0